Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	170	balint.inv.	US-PGPUB; USPAT	OR	ON	2005/10/26 11:31
L2	643	her.inv.	US-PGPUB; USPAT	OR	ON	2005/10/26 11:31
L3	8	l1 and l2	US-PGPUB; USPAT	OR	ON	2005/10/26 11:31
L4	5011	"182".clm.	US-PGPUB; USPAT	OR	ON	2005/10/26 11:31
L5	0	l3 and l4	US-PGPUB; USPAT	OR	ON	2005/10/26 11:32
L6	3929	threonine.clm.	US-PGPUB; USPAT	OR	ON	2005/10/26 11:32
L7	0	l3 and l6	US-PGPUB; USPAT	OR	ON	2005/10/26 11:32
L8	1	l1 and l6	US-PGPUB; USPAT	OR	ON	2005/10/26 11:33
L9	632	panorama.asn. or horizon.asn. or pan. asn.	US-PGPUB; USPAT	OR	ON	2005/10/26 11:34
L10	1435	l1 or l2 or l9	US-PGPUB; USPAT	OR	ON	2005/10/26 11:34
L11	1	l10 and "182".clm.	US-PGPUB; USPAT	OR	ON	2005/10/26 11:34
L12	1	l10 and threonine.clm.	US-PGPUB; USPAT	OR	ON	2005/10/26 11:35

```
            GenCore version 5.1.6
      Copyright (c) 1993 - 2005 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on: October 26, 2005, 05:19:01 ; Search time 167 Seconds
(without alignments)
377.497 Million cell updates/sec

Title: US-09-526-106b-27_COPY_1_163
Perfect score: 842
Sequence: 1 HPBTLVKVKDABDQLGARVG.........LNEAIPNDERDTTTPVAMAT 163

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	836	99.3	263	4	AAE05544	Aae05544 E. coli m
2	836	99.3	263	4	AAB36692	Aab36692 Escherich
3	836	99.3	263	8	ADJ67709	Adj67709 Escherich
4	836	99.3	264	2	AAW16634	Aaw16634 Beta-lact
5	836	99.3	264	2	AAW18680	Aaw18680 Intracell
6	836	99.3	286	2	AAR31575	Aar31575 Ampicilli
7	836	99.3	286	2	AAR97619	Aar97619 Secretory
8	836	99.3	286	2	AAR96423	Aar96423 Cytochrom
9	836	99.3	286	2	AAW16635	Aaw16635 Beta-lact
10	836	99.3	286	2	AAW18679	Aaw18679 Secretory
11	836	99.3	286	2	AAY08529	Aay08529 Vector pA
12	836	99.3	286	3	AAB10442	Aab10442 Expressio
13	836	99.3	286	3	AAB10438	Aab10438 Expressio
14	836	99.3	286	3	AAB10440	Aab10440 Expressio
15	836	99.3	286	4	AAB50898	Aab50898 Protein e
16	836	99.3	286	4	AAB31173	Aab31173 Amino aci
17	836	99.3	286	5	AAU75551	Aau75551 celZ inte
18	836	99.3	286	6	ABP55474	Abp55474 Vector pC
19	836	99.3	286	6	ABR43622	Abr43622 Cloning v
20	836	99.3	286	8	ADR70422	Adr70422 Vector pA
21	836	99.3	286	8	ADR70410	Adr70410 Vector pA
22	836	99.3	286	8	ADR70404	Adr70404 Vector pA
23	836	99.3	286	8	ADR70416	Adr70416 Vector pA
24	836	99.3	286	8	ADR70428	Adr70428 Vector pA
25	836	99.3	290	4	AAU23219	Aau23219 Novel hum
26	836	99.3	290	4	AAM84362	Aam84362 Human imm
27	836	99.3	327	2	AAW16636	Aaw16636 Beta-lact
28	836	99.3	327	2	AAW18681	Aaw18681 Membrane-
29	836	99.3	408	6	ABR55981	Abr55981 hCG beta-
30	836	99.3	585	6	ADA67747	Ada67747 Beta-lact
31	836	99.3	1031	5	ADI46109	Adi46109 Single st
32	836	99.3	1088	2	AAR88636	Aar88636 Plasmid p
33	836	99.3	1277	2	AAR52701	Aar52701 Plasmid p
34	836	99.3	2307	3	AAY70064	Aay70064 Recombina
35	836	99.3	2307	3	AAY70065	Aay70065 Recombina
36	836	99.3	2307	3	AAY70066	Aay70066 Recombina
37	836	99.3	2761	3	ADH11249	Adh11249 Vertebrat
38	835	99.2	286	2	AAY06551	Aay06551 Escherich
39	835	99.2	872	7	ADK65686	Adk65686 E coli cl
40	835	99.2	1293	7	ADC22811	Adc22811 Human G p
41	835	99.2	1293	7	ADH14284	Adh14284 Vector pC
42	835	99.2	1967	6	ABB82793	Abb82793 Amino aci
43	833	98.9	286	5	ADJ31652	Adj31652 Klebsiell
44	833	98.9	286	6	ADA67741	Ada67741 K. pneumo
45	833	98.9	583	6	ADA67745	Ada67745 Beta-lact

ALIGNMENTS

```
RESULT 1
AAE05544
ID   AAE05544 standard; protein; 263 AA.
XX
AC   AAE05544;
XX
DT   24-SEP-2001 (first entry)
XX
DE   E. coli mature TEM-1 beta-lactamase.
XX
KW   Interaction-dependent enzyme association; IdEA system; biosensor;
KW   circularly permutated interaction-activated protein; marker protein;
KW   type A beta-lactamase; TEM-1 beta-lactamase; protein-protein interaction;
KW   therapeutic; drug screening; thioredoxin; ampicillin resistance.
OS   Escherichia coli.
XX
FH   Key            Location/Qualifiers
FT   Cleavage-site  27..28
FT                  /note="Break-point between alpha and omega fragments"
FT   Region         36..40
FT                  /note="Inter-sub-domain loop"
FT   Cleavage-site  38..39
FT                  /note="Break-point between alpha and omega fragments"
FT   Active-site    45
FT   Cleavage-site  74..75
FT                  /note="Break-point between alpha and omega fragments"
FT   Cleavage-site  149..150
FT                  /note="Break-point between alpha and omega fragments"
FT   Cleavage-site  172..173
FT                  /note="Break-point between alpha and omega fragments"
FT   Region         189..204
FT                  /note="Inter-sub-domain loop"
FT   Cleavage-site  190..191
FT                  /note="Break-point between alpha and omega fragments"
FT   Cleavage-site  202..203
FT                  /note="Break-point between alpha and omega fragments"
FT   Cleavage-site  228..229
FT                  /note="Break-point between alpha and omega fragments"
PN   WO20015162 9-A2.
XX
PD   19-JUL-2001.
XX
PF   16-JAN-2001; 2001WO-US001651.
XX
PR   13-JAN-2000; 2000US-0175968P.
PR   15-MAR-2000; 2000US-0052610 6.
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2005, 05:20:11 ; Search time 16 Seconds
                                      (without alignments)
                                      980.208 Million cell updates/sec

Title: US-09-526-106B-27_COPY_1_163
Perfect score: 842
Sequence: 1 HPETLVKVKDAEDQLGARVG.........LNEAIPNDERDTTTPVAMAT 163

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_79:*
              1: pir1:*
              2: pir2:*
              3: pir3:*
              4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	836	99.3	286	2	T51301	beta-lactamase (EC
2	836	99.3	286	2	S47061	beta-lactamase (EC
3	836	99.3	286	4	S41975	beta-lactamase (EC
4	831	98.7	286	1	PNECP	penicillinase - Ba
5	831	98.7	286	4	I40905	beta-lactamase (EC
6	823	97.7	286	2	S30113	beta-lactamase (EC
7	818	97.1	286	2	S60312	extended spectrum
8	817	97.0	286	2	S60310	extended spectrum
9	817	97.0	286	2	S60311	beta-lactamase (EC
10	817	97.0	286	2	JQ1546	Bla protein - Salm
11	600	71.3	286	2	S16146	beta-lactamase (EC
12	600	71.3	286	2	A60679	beta-lactamase (EC
13	596	70.8	265	2	S00464	beta-lactamase (EC
14	596	70.8	265	2	S02434	beta-lactamase (EC
15	596	70.8	265	2	A60448	beta-lactamase (EC
16	596	70.8	286	2	A44998	beta-lactamase (EC
17	596	70.8	286	2	A60632	beta-lactamase (EC
18	596	70.8	286	2	A37200	beta-lactamase (EC
19	590	70.1	287	1	A44996	beta-lactamase (EC
20	575	68.3	279	2	A24469	beta-lactamase (EC
21	545	64.7	286	1	A44958	beta-lactamase (EC
22	463	55.0	298	2	A41381	beta-lactamase (EC
23	375.5	44.6	314	2	S06967	beta-lactamase (EC
24	370.5	44.0	302	2	S36188	beta-lactamase (EC
25	367.5	43.6	306	2	G69674	beta-lactamase (EC
26	366.5	43.5	306	2	D95395	probable Beta lact
27	365.5	43.4	281	2	S16553	beta-lactamase (EC
28	358.5	42.6	294	2	A54543	beta-lactamase (EC
29	356.5	42.3	306	1	B45822	beta-lactamase (EC
30	356	42.3	305	2	A61156	beta-lactamase (EC
31	356	42.3	305	2	A57002	beta-lactamase (EC
32	356	42.3	305	2	A60680	beta-lactamase (EC
33	355.5	42.2	291	2	S42075	beta-lactamase (EC
34	355.5	42.2	306	2	S47330	penicillinase - Ba
35	353	41.9	293	2	S04649	beta-lactamase (EC
36	352.5	41.9	311	2	JN0520	beta-lactamase (EC
37	340.5	40.4	305	1	C45822	beta-lactamase (EC
38	340	40.4	310	2	JL0091	beta-lactamase (EC
39	337.5	40.1	291	2	JP0074	beta-lactamase (EC
40	337	40.0	294	2	S44080	beta-lactamase (EC
41	332.5	39.5	306	1	PNBS5B	beta-lactamase (EC
42	332.5	39.5	306	1	PNBSU	beta-lactamase (EC
43	332.5	39.5	306	2	SO3167	beta-lactamase (EC
44	332	39.4	314	1	PNSM1U	beta-lactamase (EC
45	331.5	39.4	307	1	PNBSL	beta-lactamase (EC

ALIGNMENTS

RESULT 1
T51301
beta-lactamase (EC 3.5.2.6) - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C;Accession: T51301
R;WACH, A.; BRACHAT, A.; ALBERTISEGUI, C.; REBISCHUNG, C.; PHILIPPSEN, P.
Yeast 13, 1065-1075, 1997
A;Title: Heterologous HIS3 marker and GFP reporter modules for PCR-targeting in Saccharon
A;Reference number: Z09587
A;Accession: T51301
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-286 <WAC>
A;Cross-references: EMBL;AJ002683; PIDN:CAA05686.1
C;Genetics:
A;Gene: bla
C;Superfamily: beta-lactamase I
C;Keywords: hydrolase

Query Match   99.3%; Score 836; DB 2; Length 286;
Best Local Similarity   99.4%; Pred. No. 7.1e-71;
Matches 162; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   1 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERPPMSTFKVLLCGAVLSRID 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   24 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERPPMSTFKVLLCGAVLSRID 83

Qy   61 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   84 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143

Qy   121 KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMAT 163
           ||||||||||||||||||||||||||||||||||||||||||
Db   144 KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMAT 186

RESULT 2
S47061
beta-lactamase (EC 3.5.2.6) - phage phi-X174
C;Species: phage phi-X174
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S47061
R;Henrich, B.; Schmidtberger, B.
submitted to the EMBL Data Library, July 1994
A;Description: A variant of phiX174 gene E-based positive selection vectors with enhanced
A;Reference number: S47060
A;Accession: S47061
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-286 <HEN>
A;Cross-references: UNIPROT:Q38058; EMBL:Z35638; NID:g520996; PIDN:CAA84692.1; PID:g5209

```
                    GenCore version 5.1.6
        Copyright (c) 1993 - 2005  Compugen Ltd.

OM protein - protein search, using sw model

Run on:  October 26, 2005, 05:12:30 ; Search time 60 Seconds
                                     (without alignments)
                                     1391.148 Million cell updates/sec

Title:          US-09-526-106B-27_COPY_1_163
Perfect score:  842
Sequence:       1 HPETLVKVKDAEDQLGARVG........LNEAIPNDERDTTTPVAMAT 163

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:       1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :   UniProt_03:*
             1: uniprot_sprot:*
             2: uniprot_trembl:*

                        SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

Result No.	Score	% Query Match	Length	DB	ID	Description
1	837	99.4	286	2	Q8KMX4	escherichia
2	837	99.4	286	2	Q6ZYM6	salmonella
3	837	99.4	286	2	Q9R748	klebsiella
4	836	99.3	229	2	Q6WWY5	klebsiella
5	836	99.3	232	2	Q6WWY4	hafnia alve
6	836	99.3	241	2	Q6WWY8	klebsiella
7	836	99.3	242	2	Q6WWY3	escherichia
8	836	99.3	285	2	Q6KB67	hordeum vul
9	836	99.3	286	2	Q38058	bacteriopha
10	836	99.3	286	2	Q00626	staphylococc
11	836	99.3	286	2	Q79CL6	methylobaci
12	836	99.3	286	2	Q79DR3	escherichia
13	833	98.9	279	2	Q9X5K9	salmonella
14	833	98.9	285	2	Q6EH43	morganella
15	833	98.9	286	2	Q8KMX3	escherichia
16	833	98.9	286	2	Q8KQ72	escherichia
17	833	98.9	286	2	Q6IT48	escherichia
18	833	98.9	286	2	Q7BQ65	proteus mir
19	833	98.9	286	2	Q9AEY6	klebsiella
20	833	98.9	286	2	Q9LAC0	proteus mir
21	833	98.9	286	2	Q9R429	morganella
22	833	98.9	286	2	Q9R435	klebsiella
23	831	98.7	225	2	Q38212	bacteriopha
24	831	98.7	232	2	Q6PRU7	escherichia
25	831	98.7	255	2	Q84H50	escherichia
26	831	98.7	261	2	Q84H49	klebsiella
27	831	98.7	264	2	Q6PRU6	acinetobact
28	831	98.7	281	2	Q6QIV0	serratia ma
29	831	98.7	282	2	Q6QIV1	serratia ma
30	831	98.7	286	1	BLAT_ECOLI	escherichia
31	831	98.7	286	1	BLAT_SALTI	salmonella
32	831	98.7	286	2	O53043	klebsiella
33	831	98.7	286	2	Q8KSD3	klebsiella
34	831	98.7	286	2	Q8VP43	klebsiella
35	831	98.7	286	2	Q933Z8	escherichia
36	831	98.7	286	2	Q934D7	escherichia
37	831	98.7	286	2	Q93A77	escherichia
38	831	98.7	286	2	Q93GI3	klebsiella
39	831	98.7	286	2	Q6A253	haemophilus
40	831	98.7	286	2	Q6LBN9	pseudomonas
41	831	98.7	286	2	Q6LCV6	neisseria g
42	831	98.7	286	2	Q6TMH1	streptococc
43	831	98.7	286	2	Q6UVM7	acinetobact
44	831	98.7	286	2	Q6W7J4	escherichia
45	831	98.7	286	2	Q6W9J1	enterobacte

```
                        ALIGNMENTS

RESULT 1
Q8KMX4
ID   Q8KMX4      PRELIMINARY;      PRT;   286 AA.
AC   Q8KMX4;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   TEM-93 ES-beta-lactamase.
GN   Name=bla-TEM-93;
OS   Escherichia coli.
OG   Plasmid pblaTEM-93.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ClSiS 3445/98;
RA   Baraniak A.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ClSiS 3445/98;
RA   Gniadkowski M.;
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ318093; CAC85560.1; -.
DR   HSSP; Q9R435; 1HT2.
DR   InterPro; IPR001466; Beta_lactamase.
DR   InterPro; IPR000871; Beta_lactamase_A.
DR   Pfam; PF00144; Beta-lactamase; 1.
DR   PRINTS; PR00118; BLACTAMASEA.
DR   PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW   Plasmid.
SQ   SEQUENCE   286 AA;  31514 MW;  1555DCE499016FB8 CRC64;

Query Match             99.4%;  Score 837;  DB 2;  Length 286;
Best Local Similarity   98.8%;  Pred. No. 1.1e-65; -.
Matches  161;  Conservative   1;  Mismatches   1;  Indels   0;  Gaps   0;

Qy    1 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMSTFKVLLCGAVLSRID 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db   24 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMSTFKVLLCGAVLSRVD 83

Qy   61 AGQEQLGRRIHYSQNDLVEYSPVTEKGHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   84 AGQEQLGRRIHYSQNDLVEYSPVTEKGHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGP 143

Qy  121 KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMAT 163
          |||||||||||||||||||||||||||||||||||:||
Db  144 KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPAAMAT 186

RESULT 2
Q6ZYM6
ID   Q6ZYM6      PRELIMINARY;      PRT;   286 AA.
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2005, 05:22:11 ; Search time 22 Seconds
(without alignments)
553.082 Million cell updates/sec

Title: US-09-526-106B-27_COPY_1_163
Perfect score: 842
Sequence: 1 HPETLVKVKDAEDQLGARVG.........LNEAIPNDERDTTTPVAMAT 163

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 segs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	836	99.3	286	1	US-07-721-775A-2	Sequence 2, Appli
2	836	99.3	286	1	US-08-339-658-2	Sequence 2, Appli
3	836	99.3	286	3	US-09-263-933-7	Sequence 7, Appli
4	836	99.3	286	3	US-09-263-933-14	Sequence 14, Appl
5	836	99.3	286	3	US-09-263-933-21	Sequence 21, Appl
6	836	99.3	286	3	US-09-025-769B-265	Sequence 265, App
7	836	99.3	286	3	US-09-025-769B-362	Sequence 362, App
8	836	99.3	286	4	US-09-919-901-7	Sequence 7, Appli
9	836	99.3	286	4	US-09-919-901-14	Sequence 14, Appl
10	836	99.3	286	4	US-09-919-901-21	Sequence 21, Appl
11	836	99.3	286	4	US-09-490-070A-265	Sequence 265, App
12	836	99.3	286	4	US-09-490-070A-362	Sequence 362, App
13	836	99.3	286	4	US-09-490-153-265	Sequence 265, App
14	836	99.3	286	4	US-09-490-153-362	Sequence 362, App
15	836	99.3	286	4	US-10-191-966-7	Sequence 7, Appli
16	836	99.3	286	4	US-10-191-966-14	Sequence 14, Appl
17	836	99.3	286	4	US-10-191-966-21	Sequence 21, Appl
18	836	99.3	286	4	US-09-490-324-265	Sequence 265, App
19	836	99.3	286	4	US-09-490-324-362	Sequence 362, App
20	836	99.3	299	3	US-09-025-769B-285	Sequence 285, App
21	836	99.3	299	3	US-09-025-769B-298	Sequence 298, App
22	836	99.3	299	3	US-09-025-769B-300	Sequence 300, App
23	836	99.3	299	4	US-09-490-070A-285	Sequence 285, App
24	836	99.3	299	4	US-09-490-070A-298	Sequence 298, App
25	836	99.3	299	4	US-09-490-070A-300	Sequence 300, App
26	836	99.3	299	4	US-09-490-153-285	Sequence 285, App
27	836	99.3	299	4	US-09-490-153-298	Sequence 298, App
28	836	99.3	299	4	US-09-490-153-300	Sequence 300, App
29	836	99.3	299	4	US-09-490-324-285	Sequence 285, App
30	836	99.3	299	4	US-09-490-324-298	Sequence 298, App
31	836	99.3	299	4	US-09-490-324-300	Sequence 300, App
32	836	99.3	2307	3	US-09-263-933-2	Sequence 2, Appli
33	836	99.3	2307	3	US-09-263-933-9	Sequence 9, Appli
34	836	99.3	2307	3	US-09-263-933-16	Sequence 16, Appl
35	836	99.3	2307	4	US-09-919-901-2	Sequence 2, Appli
36	836	99.3	2307	4	US-09-919-901-9	Sequence 9, Appli
37	836	99.3	2307	4	US-09-919-901-16	Sequence 16, Appl
38	836	99.3	2307	4	US-10-191-966-2	Sequence 2, Appli
39	836	99.3	2307	4	US-10-191-966-9	Sequence 9, Appli
40	835	99.3	2307	4	US-10-191-966-16	Sequence 16, Appl
41	835	99.2	286	4	US-09-555-510B-9	Sequence 9, Appli
42	835	99.2	286	4	US-10-231-013-9	Sequence 9, Appli
43	835	99.2	1293	4	US-09-170-496D-292	Sequence 292, App
44	835	99.2	1293	4	US-09-364-425B-57	Sequence 57, Appl
45	831	98.7	263	1	US-08-407-544-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-07-721-775A-2
; Sequence 2, Application US/07721775A
; Patent No. 5180666
; GENERAL INFORMATION:
; APPLICANT: States, J. Christopher
; APPLICANT: Hines, Ronald N.
; TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
; TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard, Perry & Milton
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/721,775A
; FILING DATE: 19910627
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-321WSU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (313) 689-3554
; TELEFAX: (313) 689-4071
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-721-775A-2

Query Match 99.3%; Score 836; DB 1; Length 286;
Best Local Similarity 99.4%; Pred. No. 7e-91;
Matches 162; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy   1 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  24 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRID 83
```

OM protein - protein search, using sw model

Copyright   GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.

Run on: October 26, 2005, 05:29:12 ; Search time 68 seconds (without alignments) 1000.798 Million cell updates/sec

Title: US-09-526-106B-27_COPY_1_163
Perfect score: 842
Sequence: 1 HPETLVKVKDAEDQLGARVG........LNEAIPNDERDTTTPVAMAT 163

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 1862994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

```
 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	836	99.3	263	15	US-10-668-778-2	Sequence 2, Appli
2	836	99.3	286	10	US-09-919-901-7	Sequence 7, Appli
3	836	99.3	286	10	US-09-919-901-14	Sequence 14, Appl
4	836	99.3	286	11	US-09-837-306-354	Sequence 354, App
5	836	99.3	286	14	US-10-191-966-7	Sequence 7, Appli
6	836	99.3	286	14	US-10-191-966-14	Sequence 14, Appl
7	836	99.3	286	14	US-10-191-966-21	Sequence 21, Appl
8	836	99.3	286	15	US-10-045-674-523	Sequence 523, App
9	836	99.3	286	16	US-10-416-708A-73	Sequence 73, Appl
10	836	99.3	286	10	US-09-919-901-2	Sequence 2, Appli
11	836	99.3	2307	10	US-09-919-901-2	Sequence 2, Appli
12	836	99.3	2307	10	US-09-919-901-9	Sequence 9, Appli
13	836	99.3	2307	10	US-09-919-901-16	Sequence 16, Appl
14	836	99.3	2307	14	US-10-191-966-2	Sequence 2, Appli
15	836	99.3	2307	14	US-10-191-966-9	Sequence 9, Appli
16	836	99.3	2307	14	US-10-191-966-16	Sequence 16, Appl
17	835	99.2	286	14	US-10-231-013-9	Sequence 9, Appli
18	835	99.2	286	16	US-10-842-534-9	Sequence 9, Appli
19	835	99.2	1293	14	US-10-251-385-292	Sequence 292, App
20	835	99.2	1293	18	US-10-668-035-57	Sequence 57, Appl
21	835	99.2	1967	16	US-10-477-044-1	Sequence 1, Appl
22	831	98.7	265	9	US-09-772-114-6	Sequence 6, Appli
23	831	98.7	265	14	US-10-280-482-2	Sequence 2, Appli
24	831	98.7	265	17	US-10-656-029-2	Sequence 2, Appli
25	831	98.7	285	9	US-09-772-114-7	Sequence 7, Appli
26	831	98.7	286	14	US-10-016-668-5	Sequence 5, Appli
27	831	98.7	286	14	US-10-280-482-4	Sequence 4, Appli
28	831	98.7	286	17	US-10-656-029-4	Sequence 4, Appli
29	831	98.7	286	17	US-10-877-952-26	Sequence 26, Appl
30	831	98.7	286	17	US-10-877-952-71	Sequence 71, Appl
31	831	98.7	286	20	US-11-059-226-34	Sequence 34, Appl
32	831	98.7	286	20	US-11-059-226-35	Sequence 35, Appl
33	831	98.7	286	20	US-11-059-226-36	Sequence 36, Appl
34	831	98.7	673	18	US-10-450-763-58554	Sequence 58554, A
35	831	98.7	1575	18	US-10-450-763-58292	Sequence 58292, A
36	828	98.3	264	17	US-10-877-952-18	Sequence 18, Appl
37	828	98.3	362	15	US-10-469-199-2	Sequence 2, Appli
38	828	98.3	584	17	US-10-890-675-2	Sequence 2, Appli
39	824	97.9	265	9	US-09-772-114-8	Sequence 8, Appli
40	824	97.9	265	14	US-10-280-482-6	Sequence 6, Appli
41	824	97.9	265	16	US-10-622-088-114	Sequence 114, App
42	824	97.9	265	17	US-10-656-029-6	Sequence 6, Appli
43	824	97.9	265	17	US-10-877-952-154	Sequence 154, App
44	824	97.9	265	20	US-11-040-924-1	Sequence 1, Appl
45	823	97.7	264	9	US-09-772-114-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-10-668-778-2
```
; Sequence 2, Application US/10668778
; Publication No. US20040038317A1
; GENERAL INFORMATION:
; APPLICANT: Balint, Robert F.
; APPLICANT: Her, Jeng-Horng
; APPLICANT: KaloBios, Inc.
; TITLE OF INVENTION: Interaction-Activated Proteins
; FILE REFERENCE: 021167-000700US
; CURRENT APPLICATION NUMBER: US/10/668,778
; CURRENT FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: US/09/526,106
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: US 60/124,339
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: US 60/135,926
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: US 60/175,968
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; OTHER INFORMATION: TEM-1 beta-lactamase
US-10-668-778-2
```

Query Match 99.3%; Score 836; DB 15; Length 263;
Best Local Similarity 99.4%; Pred. No. 7.8e-83;
Matches 162; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

  http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.